

Figure 1

$\xrightarrow{1}$
1 ACGAGGGAAGGAGGCACACCCGGGGTGGCGCAGTGAGGAGGGGCGCGACGGCCA
58 GGAGGCTGGTGGAGCGACACCCAGGCAGGAGAGGGGAAGAACTCTCTCCCTTCTGAAC
118 CCCCTTTCCTTGAGAGACGAGTTGGGGAGTCCACGCATTACCCACTCGGGCCGCA
178 AAACCTCCCTTCTTAGCCCTCTGCCCCCGCCCTTGCTTATAAGCCTTTGAGACCGCAGA
 $\xrightarrow{2}$
238 AGGACCTTGTGTGGAACGGGACGGCCAAGAGGAAGCCAGATCGCTGAGGTCGGTCT
298 CCAGTTGCCTCCTGCTATATCCATTGGAAGAGAAAGTTGTGACTTGGGCCCCAAGT
 $\xrightarrow{3}$
358 TTTGAGAGAACTGGGCTTTCGGCGGGGGACAGAGGAGGCTCGTGGGAGCTTTCCCC
418 ATGGAGCTTACCCAGCCTGCAGAAGACCTCATCCAGACCCAGCAGACCCCTGCCTCAGAA
1 M E L T Q P A E D L I Q T Q Q T P A S E
478 CTTGGGACCTGAAGACCCCGAGAGGAGGCTGCAGATGGCTCAGACACTGTGGTCCTC
21 L G D P E D P G E E A A D G S D T V V L
538 AGTCTCTTTCCTGCACCCCTGAGCCTGTGAATCCTGAACCGGATGCCAGTGTTCCTCT
41 S L F P C T P E P V N P E P D A S V S S
 $\xrightarrow{4}$
598 CCACAGGcagGAGCTCCCTGAAGCACTCCACCACTCTCACCAACCGGAGGGAAC
61 P Q (A) G S S L K H S T T L T N R Q R G N

Figure 2a

658 GAGTGTGAGCTCTGCCGGCCACCTAGACTCCCTGTCCATCCACCAGCTCGCAGCACAG
 81 E V S A L P A T L D S L S I H Q L A A Q
 718 GGGAGCTGACAGCTGAAGGAGCATTTGCGGAAGGTGACAACCTCGTCAACAAGCCA
 101 G E L D Q L K E H L R K G D N L V N K P
 778 GACGAGCGGGCTTCACCCCTCATCTGGCCCTCCGCCCTTTGGAGAGATTGAGACCGTT
 121 D E R G F T P L I W A S A F G E I E T V
 838 CGCTTCCTGCTGAGTGGGTGCCGACCCACATCCTGGCAAAGAGCGAGAGCGGCC
 141 R F L L E W G A D P H I L A K E R E S A
 898 CTGTCGCTGGCCAGCACAGGCGGCTACACAGACATTGTGGGGCTGCTGTGAGCGGTGAC
 161 L S L A S T G G Y T D I V G L L L E R D
 958 GTGGACATCAACATCTATGATTGGAATGAGGGACGCCACTGCTGTACGCTGTGCGCGGG
 181 V D I N I Y D W N G G T P L L Y A V R G
 1018 AACCACGTGAAATGCGTTGAGGCCTTGCTGGCCCGAGGCGGTGACCTCACCCGAGGCC
 201 N H V K C V E A L L A R G A D L T T E A
 1078 GACTCTGGCTACACCCCGATGACCTTGCCGTGGCCCTGGGATACCGGAAGTGCAACAG
 221 D S G Y T P M D L A V A L G Y R K V Q Q

Figure 2b

1138 GTGATCGAGAACCATCCTCAAGCTCTTCCAGAGCAACCTGGTGCCCGCTGACCCCTGAG
241 V I E N H I L K L F Q S N L V P A D P E
1198 TGAAGGCCGCCCTGCCGGGACTCAGACACTCAGGGAACAATGGTCAGCCAGAGCTGGG
260 *
1258 GAAACCCAGAACTGACTTCAAAGGCAGCTTCTGGACAGGTGGTGGAGGGACCCCTTCCC
1318 AAGAGGAACCAATAAACCTTCTGTGCAG - polyA

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Figure 2c

sREXANK	MELTQPAEDLIQTQTPASELGDPEDEEADGSDTVVLSLFPCTPEPVNPEPDASVSS	60
mREXANK	--P--V--N--VPN--P--VPD-E-----TRD-SPEN-----DA-----A-----A--	60
s homol	NAFNVFTEVFHLAECNIHTSPSPGIGQVRHVXTP-T	35
m homol	ASVLEKAECNIHTSPSPGIGQVRHVYTP-T	29
sREXANK	HHHHT HHHHHHHHHHT	113
mREXANK	PQaGSSLKHSTLTNRQRGNEVSALPATLSLHQLAQGELDQLKEHLRKG.....	119
s homol	L--F-----S-----D-----acpactc	87
m homol	TKHF-PI-Q-----TT-LLAN---V-----MLY-ATRIEQ.....	81
ABPβ	TKHF-PI-Q-----TT-LLAN---A-----MLY-ATRIEQ.....	25
sREXANK	TT HHHHHHHHT HHHHHHHHTT TT TT HHHHHHHHT H	170
mREXANK	...DNLVKNPDERGETPLIWASAFGEIETVRFLEWGAADPHILAKERESALSTGGYT	179
s homol	lsgN--I-----D-----M-----	144
m homol	...E-VI-HT--E-----M--A-H-Q-AV-E---QN---QL-G-G-----CSK---	138
ABPβ	...E-VI-HT--E-----M--A-H-Q-AV-E---QN---QL-G-G-----CSK---	80
sREXANK	...APETT..-WL-TS--HL-AQY-HFS-TEV--RA-VSRDART-VDRTP-HM-ASE-HA	80

Figure 3a

	ank 2	ank 3	
HsREFXANK	HHHHHHHTT TT TTT HHHHHHHTT HHHHHHHTT TT TTT HHHHH		230
MmREFXANK	DIVGLLERDVIDINIYDNGGTPLLYAVRGNHVKCVEALLARGADLTTEADSGYTPMDLA		239
Hs homol	---R---D-----		204
Mm homol	---XM---DCG---V-X-----H-----KM---ES---P-I-T-----NS---		198
GABPβ	---KM---DCG---V-E-----GH-----KM---EN---P-I-T-----NS---		140
	N---EV---KHGA-V-AK-MLKM-A-HW-TEH---QEV---L-IKY---VH-QSKFCK-AF-IS		

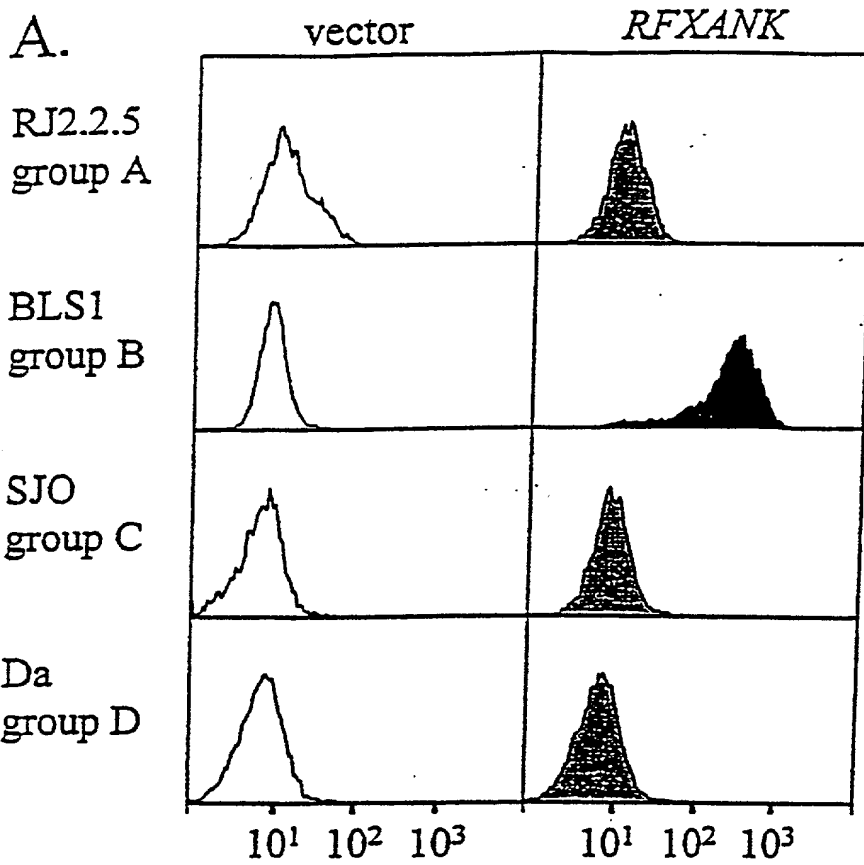
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HsREFXANK	HHTT HHHHHHH	
MmREFXANK	VALGYRKVQVQVIENHILKLFQSNLVPADPE	260
Hs homol	-----M-S---R-----T-G-V---	269
Mm homol	-----IEVFNRLSHIC	220
GABPβ	-----GCSDYMLVTDVERI	218
	IDN-NEDLAEILQ	153

Figure 3b

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A.



B.

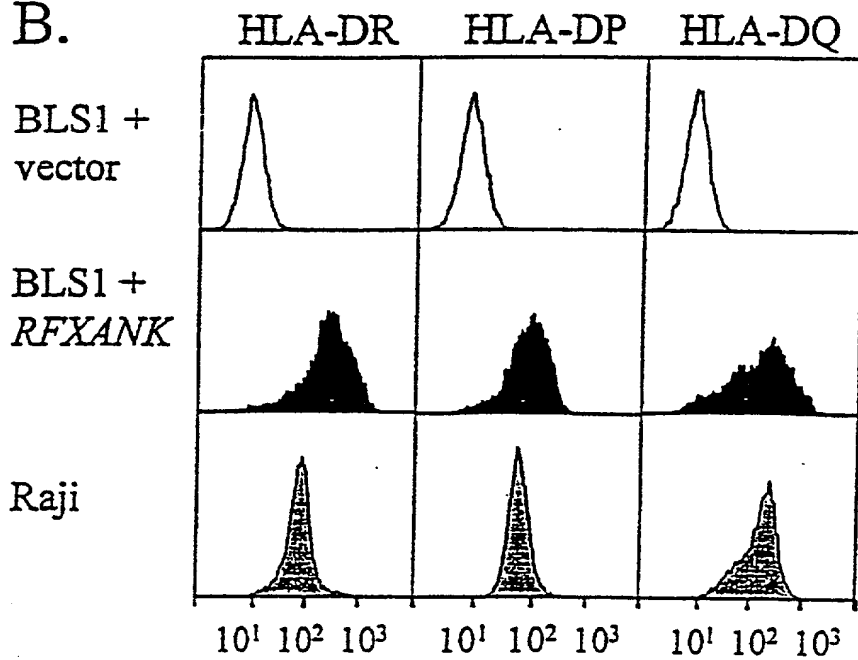
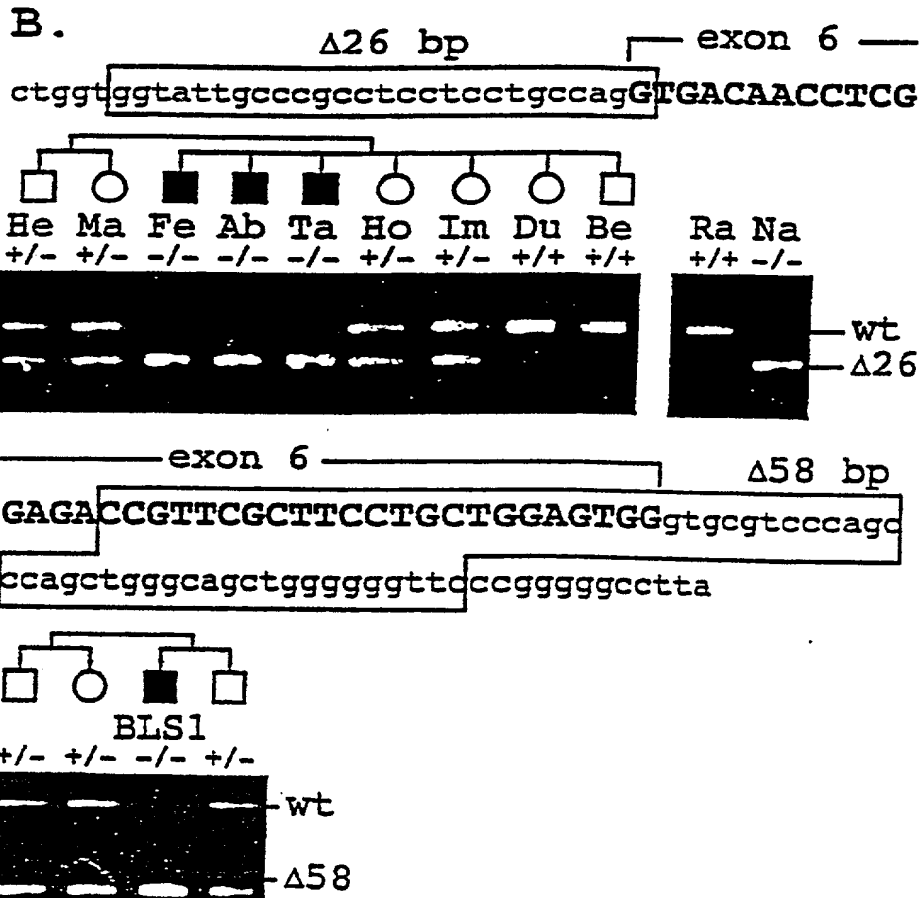
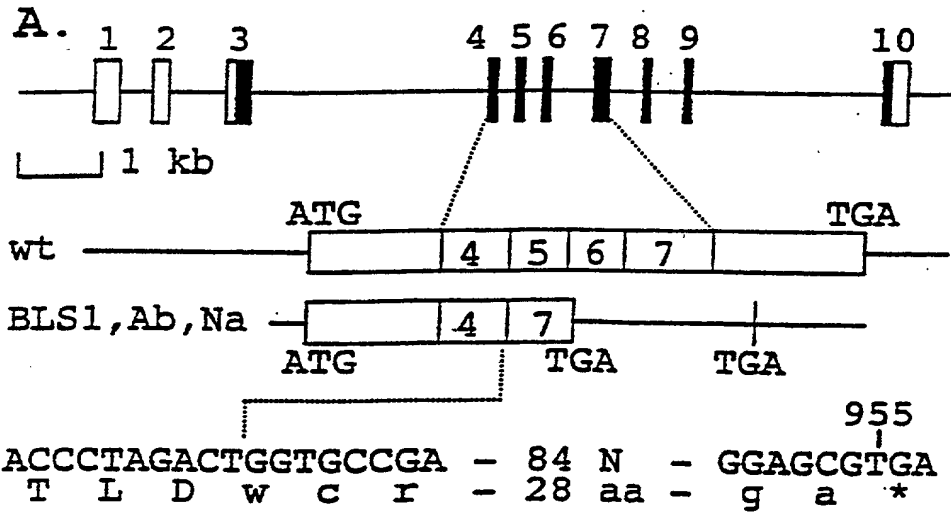


Figure 4

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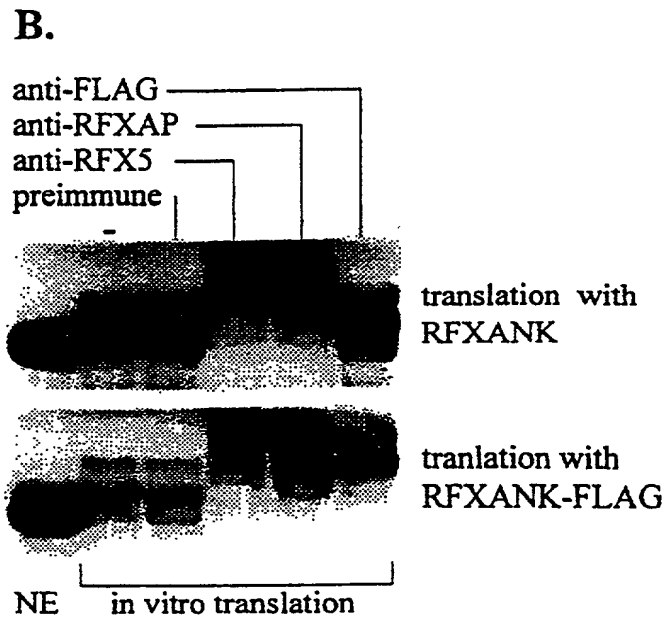
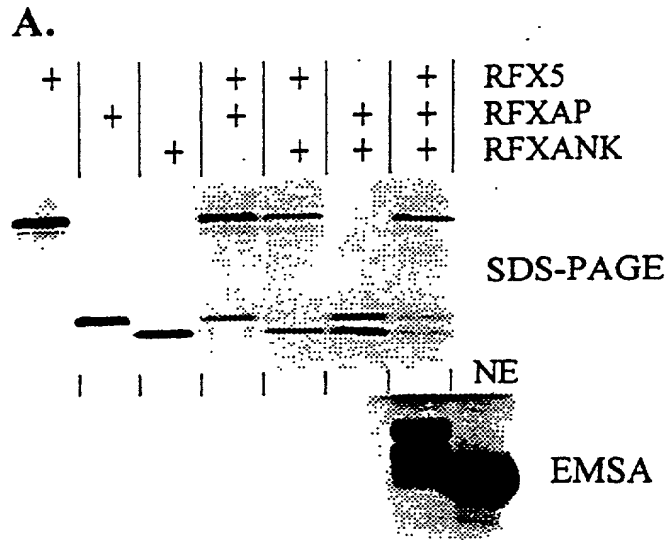


Figure 6

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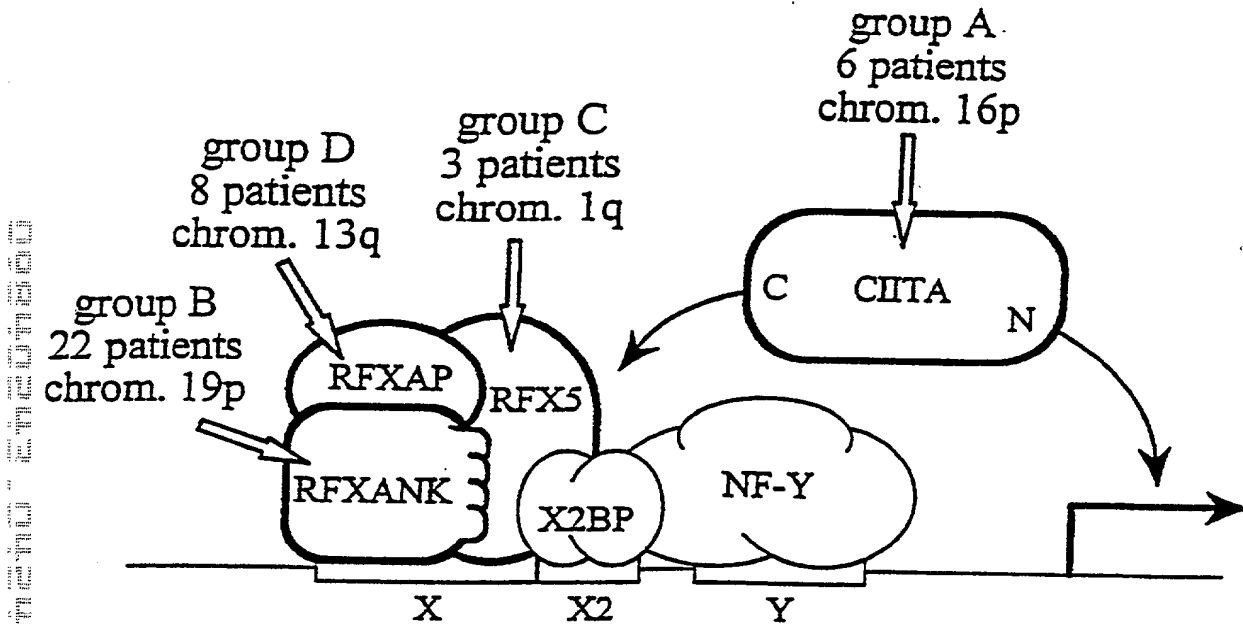


Figure 7

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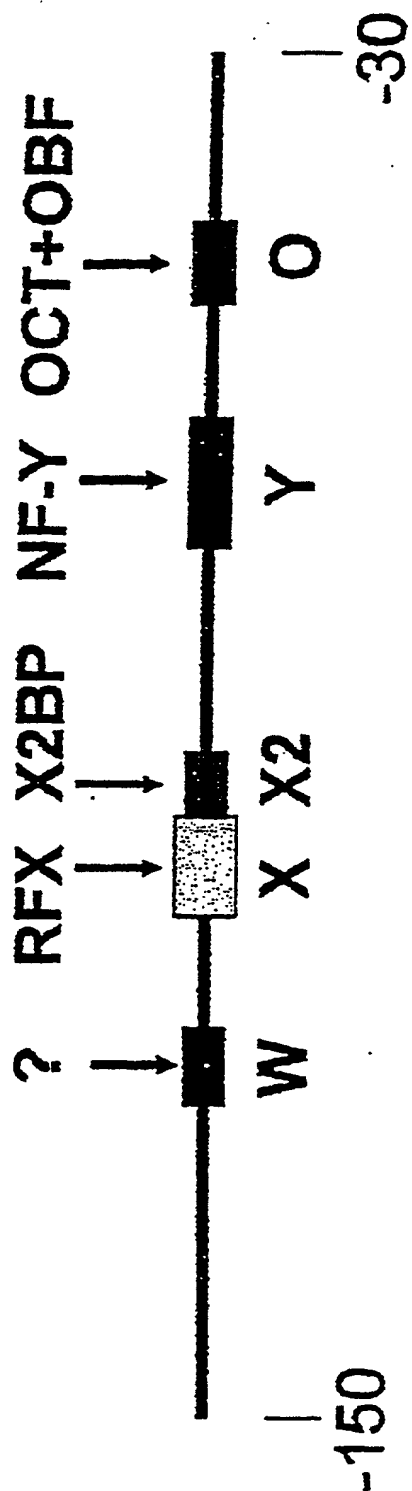


Figure 8

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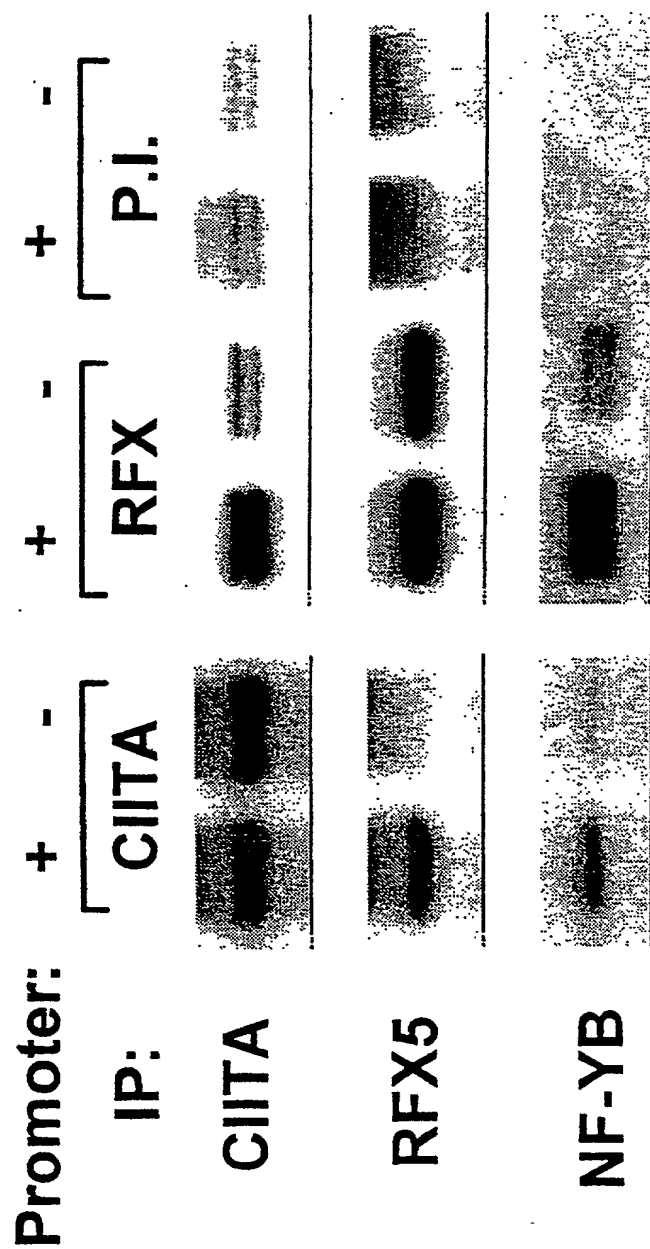


Figure 9

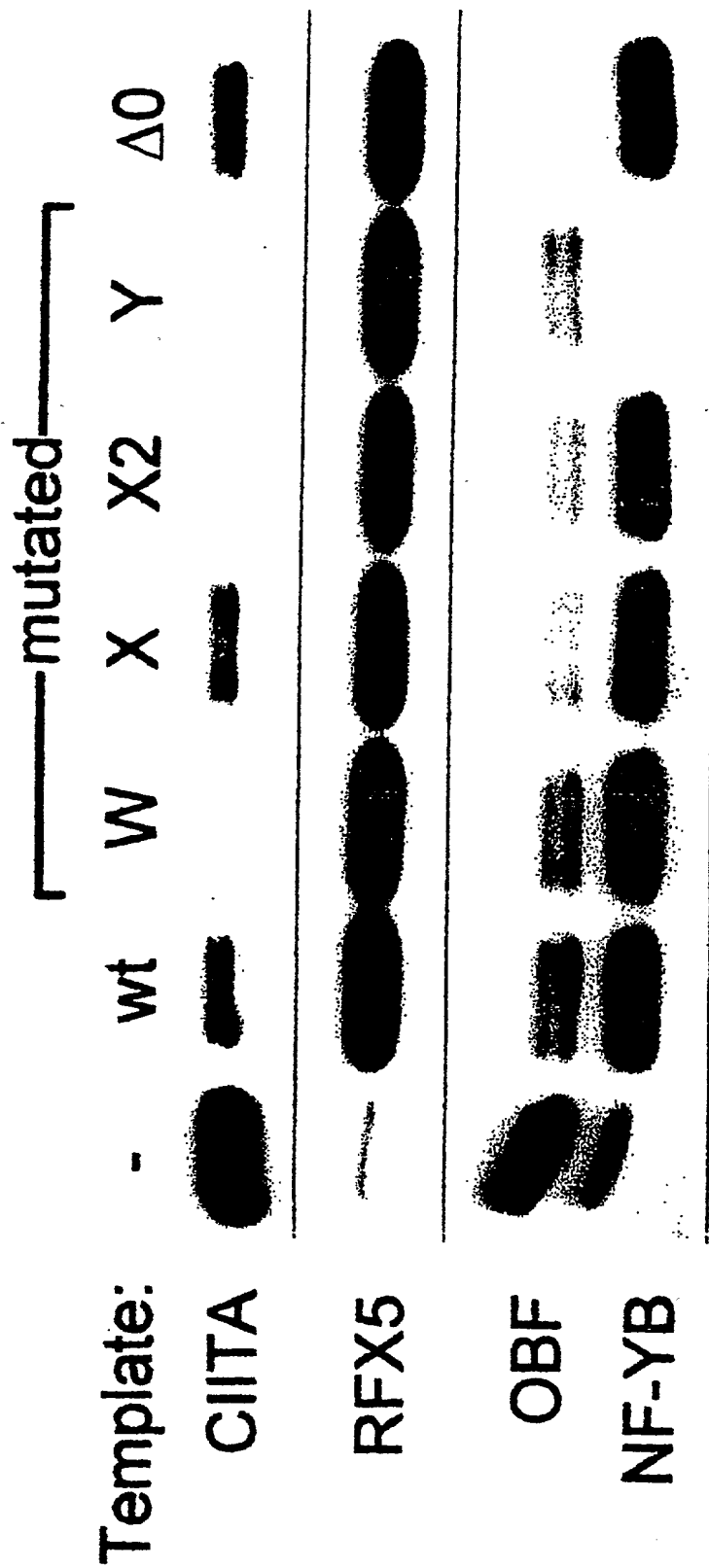


Figure 10a

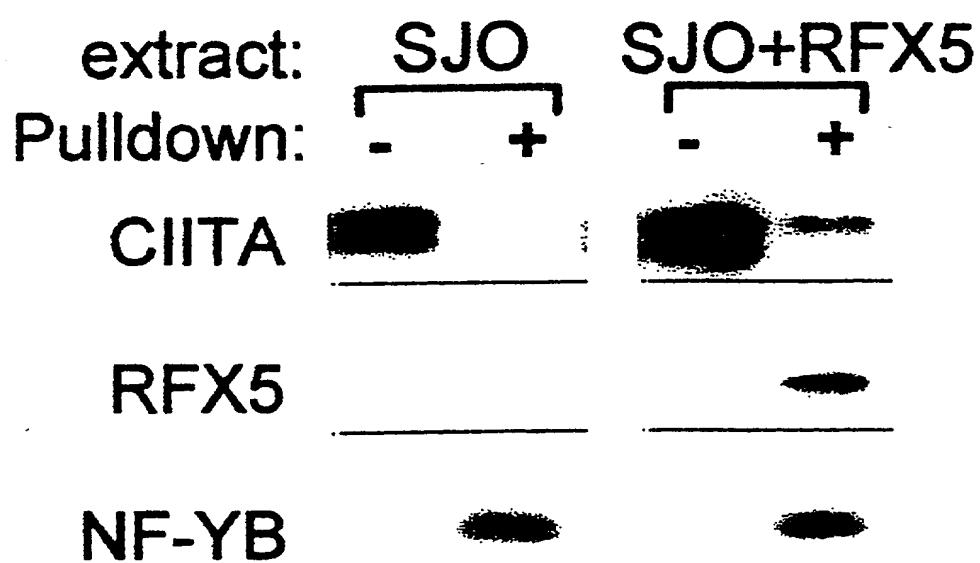


Figure 10b

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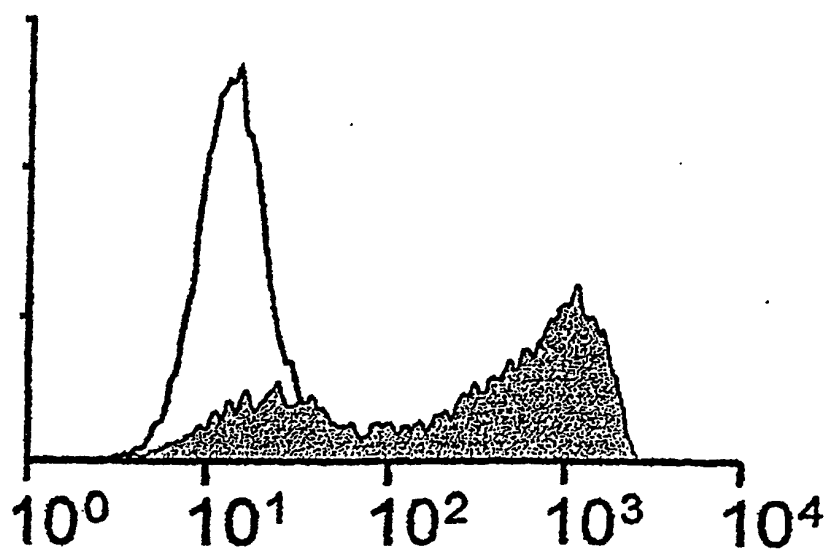


Figure 10c

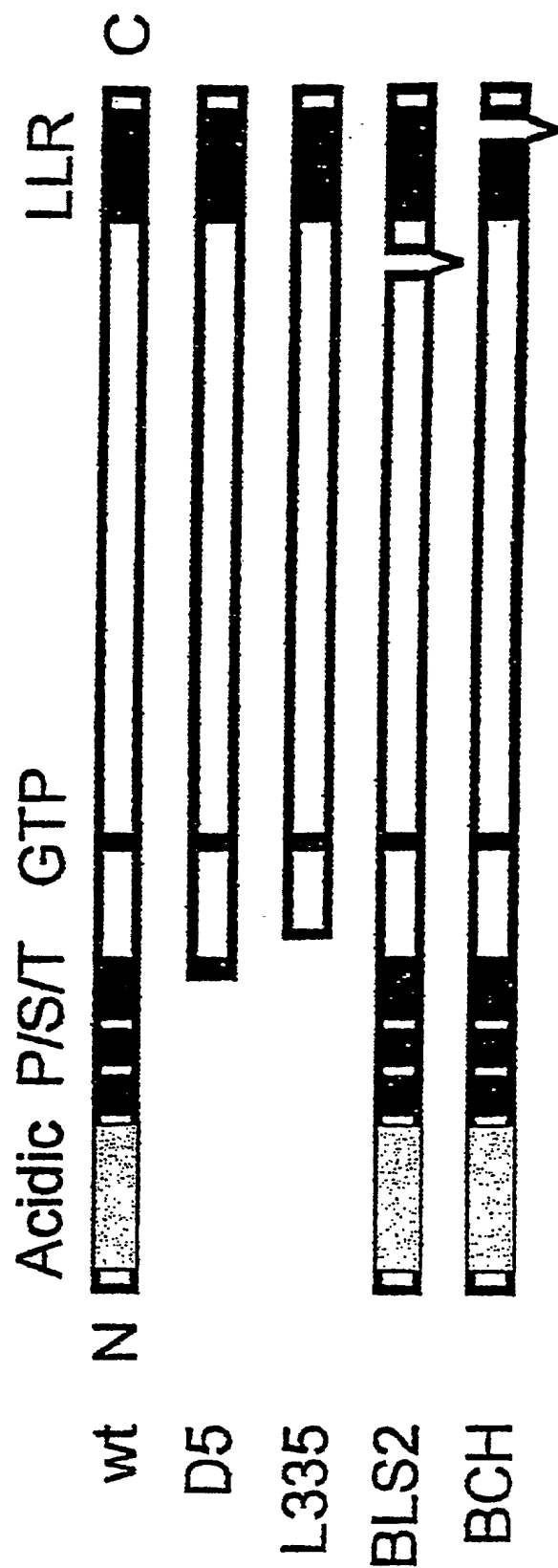


Figure 11a

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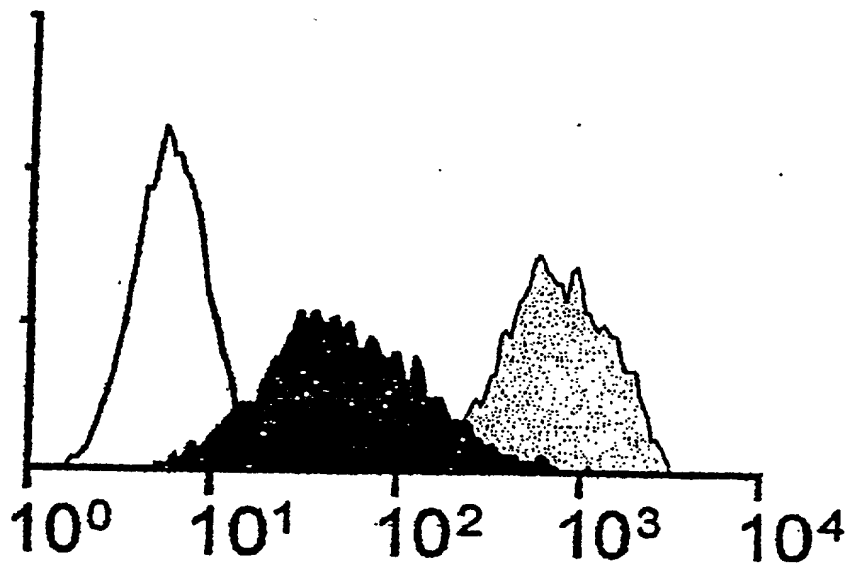


Figure 11b

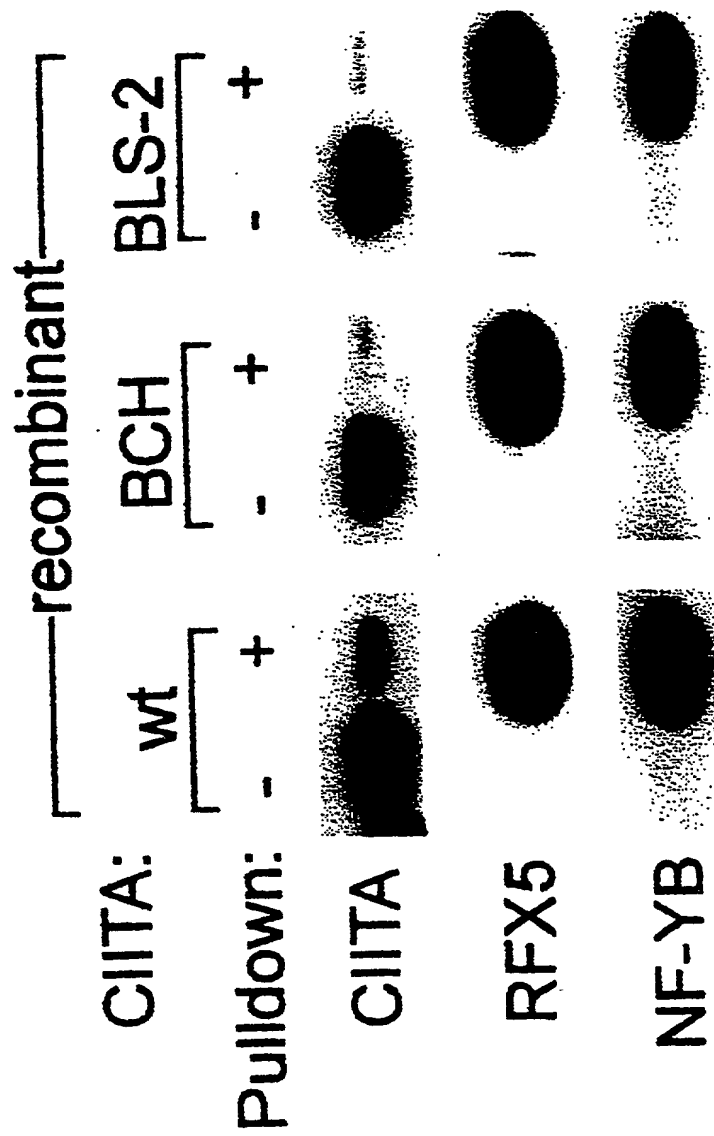


Figure 11d